1813/424/277.1

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#### FIGURE 1

Caputa 1 of 48

2 3 MK 200KD— 100.5KD— 72KD— 43KD— 28.5KD— 1 - anti- EGFr PoAB RK-2 2 - Cyt-356 MoAB/RAM 3 - RAM

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FIGURE 2A FIGURE 2B

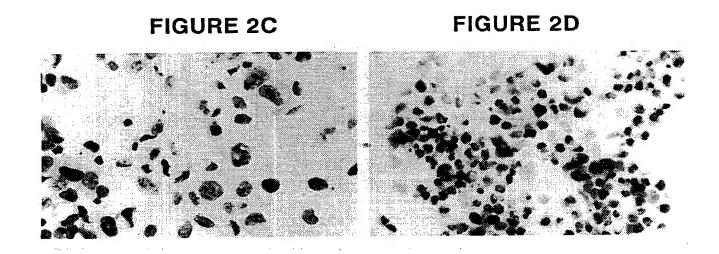


FIGURE 3A

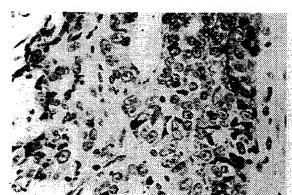


FIGURE 3B

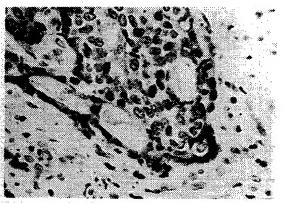


FIGURE 3C

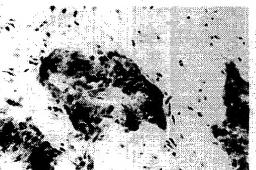
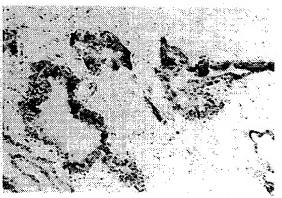


FIGURE 3D

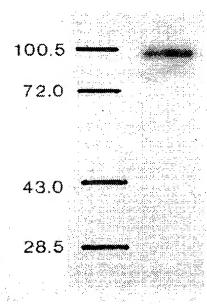


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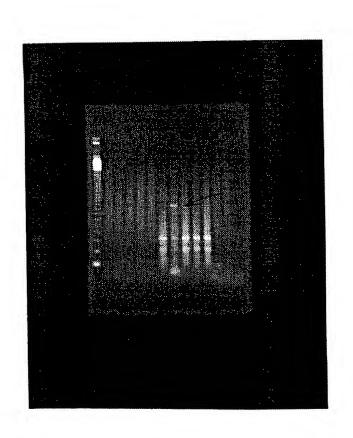
WO 94/09820

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#### FIGURE 4

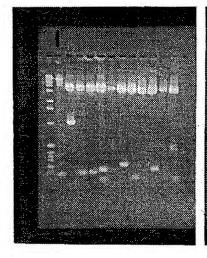


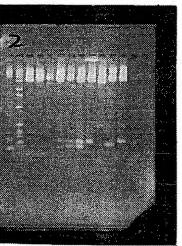
5/48 FIGURE 5



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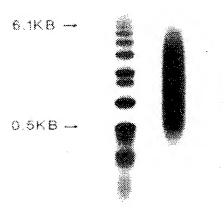
FIGURE 6A FIGURE 6B





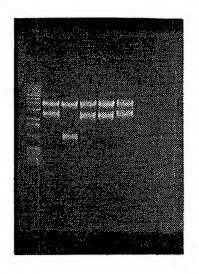
7/48

#### FIGURE 7

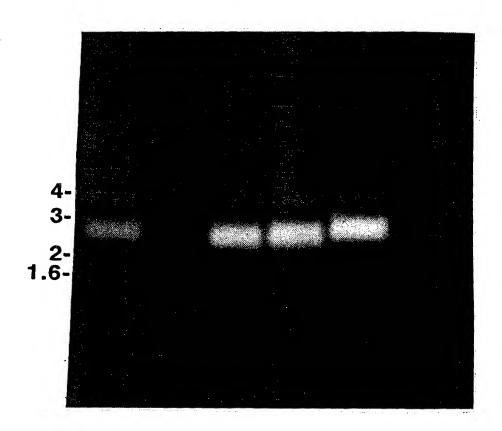


8/48

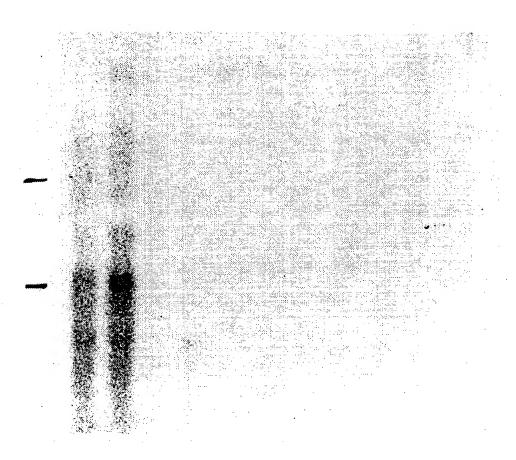
#### FIGURE 8



9/48 FIGURE 9



10/48 FIGURE 10



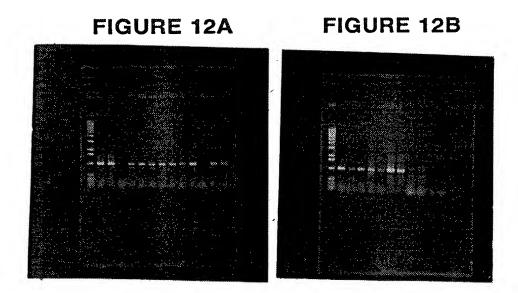
11/48 FIGURE 11

1 2 3
9.5\_\_
7.5\_\_
4.4\_\_

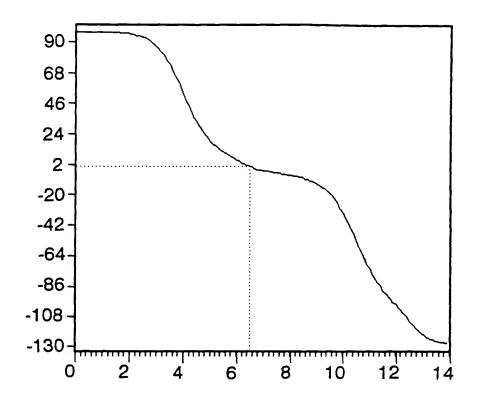
2.4\_\_

1.4\_\_

12/48



13/48 FIGURE 13



Done on sequence PMSANTIGEN. Total number of residues is: 750. Analysis done on the complete sequence.

41.2% 2% 8 î Â **A** î AA AA 264 309 76 101 CNAT CNAT CNAT -75 -88 00 II Ħ II 11 conformation conformation conformation conformation E E E C Extended Helical Turn Coil In

14/48

Sequence shown with conformation codes.

are given conformation Ø in or more residues വ Consecutive stretch of overlined

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PCT/US93/10624

**NITPKHNMKAFLDELKAENIKKFLYNFTQIPHLAGTEQNFQLAKQIQSQW** 

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50

Extended conformation: conformation: 100 **MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEAT** X<\*\*\*\*\*XXXXXX----X<\*\*\*\*\*XXXXXX--Symbols used in the semi-graphical representation: 90 FIGURE 14-4 30 80 ----<<---XXXXXXXXXXXXXXXX conformation: conformation: Semi-graphical output. ---< 20 9 Helical Turn

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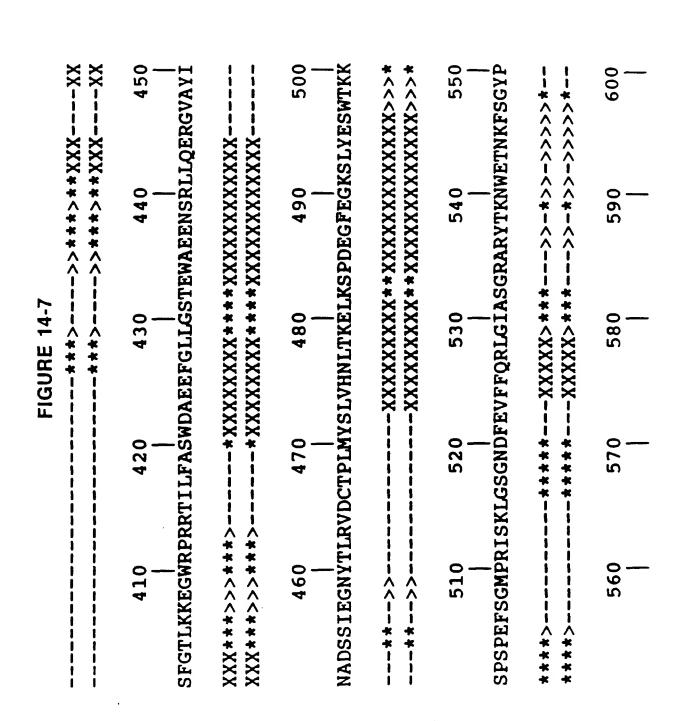
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150 200 **KEFGLDSVELAHYDVLLSYPNKTHPNYISIINEDGNEIFNTSLFEPPPPG YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKI** 140 190 130 180 170 120 110 160

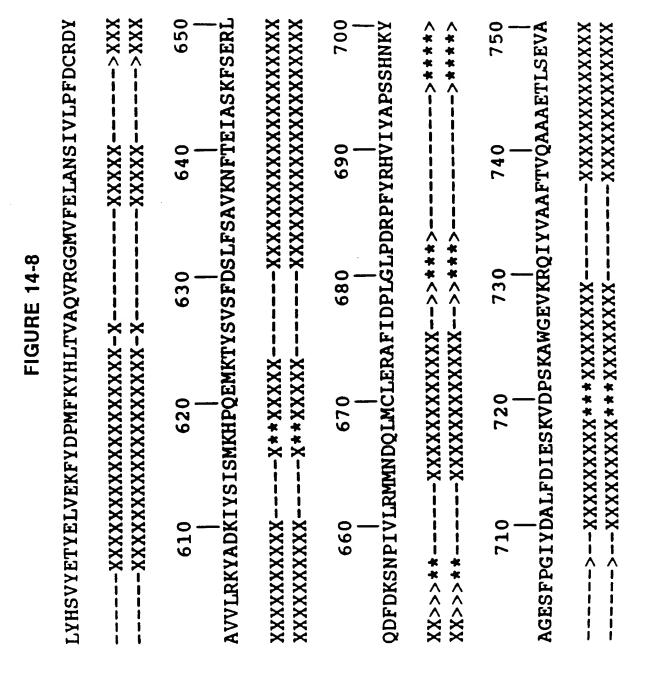
SUBSTITUTE SHEET (RULE 26)

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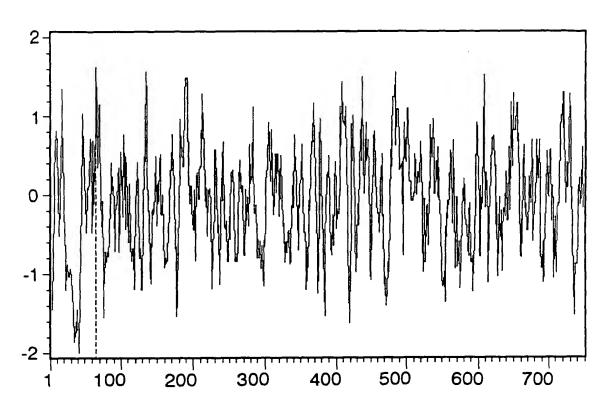
<u> </u>	250   LPG	^ ^ * *	300     		350   STN	* *	400    IVR
-<< <xxxxxxxxxxxxxxxxxxxxx-< td=""><td>240   GVKSYPDGWN</td><td><pre>&lt;**-&lt;&lt;&lt;</pre></td><td>290   GLPSIPVHPI</td><td>* *</td><td>340   STQKVKMHIH</td><td>*XXXXXX*-</td><td>390   PQSGAAVVHE</td></xxxxxxxxxxxxxxxxxxxxx-<>	240   GVKSYPDGWN	<pre>&lt;**-&lt;&lt;&lt;</pre>	290   GLPSIPVHPI	* *	340   STQKVKMHIH	*XXXXXX*-	390   PQSGAAVVHE
XXXXXX	2 ADYFAPG		2 SIAEAVG		3 SFTGNFS	X *   *	3 VFGGIDP
14-6 XX> XX>	230   ILYSDPA	·	280   EYAYRG	XX	330   PYNVGPC		380   GHRDSWI
FIGURE -**>***	220   VKNAQLAGAKGV	XXXXXXXX**<<	270   AGDPLTPGYPAN	****	320   PPDSSWRGSLKV		370    GAVEPDRYVILG
	210 220 230 240 250             VIARYGKVFRGNKVKNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNLPG	*^^	260 270 280 290 300           GGVQRGNILNLNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIGYY	^^ <del>*</del> ^	310 320 330 340 350             DAQKLLEKMGGSAPPDSSWRGSLKVPYNVGPGFTGNFSTQKVKMHIHSTN	XXXXXXX->>>++++><-XXXXXXXXXXXX	360 370 380 390 400           EVTRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHEIVR



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PCT/US93/10624

FIGURE 15B

Done on sequence PMSANTIGEN. Total number of residues is: 750. Analysis done on the complete sequence.

-> This is the value recommended by the authors The averaging group length is: 6 amino acids. The method used is that of Hopp and Woods.

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The three highest points of hydrophilicity are:

Asp-Glu-Leu-Lys-Ala-Glu Asn-Glu-Asp-Gly-Asn-Glu Lys-Ser-Pro-Asp-Glu-Gly 68 137 487 to to to 132 482 From From From 1.57 1.55 1.62

Ah stands for: Average hydrophilicity.

control proteins, only the highest point was in 1001 and third point: a known antigenic group. The second of incorrect predictions Note that, on a group of proportion of 33% of the cases assigned to gave a

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1240 CCCTA	:: 5 :: 5 :: 5 :: 5 :: 5 :: 5 :: 5 :: 5	1200 00 CCAC	: :: ::: STGAACAATTCCA 1250 12	360 TGGAA ::: AAGAA	420 TTGA : : CTAA 1370
12 3CC	r T	1300 1300	: GT	1360 GTGG : : GAAG	1420 ATTG. : GCTA. 137
GTC		CAC	:: :: :: :: : : : : : : : : : : : : :	1340 1350 1360 1370  TAGGTACTCTCAGAGGAGCAGTGGGAACCAGACAGATATG ::::::::::::::::::::::::::::::::	GGT STG
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, AA	TG	AG	ີ:	rci : : rat	3GT
AGG	AGG	AAA	:: 4AT )	: :	.: .: TGC
1220 GGAG	X	1280 CACA	: : A-TA 1230	340 AGGT ::: CGGT 1290	400 CTCA ::: CTCC
12 TGC	:::: TGGA	112 ACA	4GA 1	1340 VTAGG : :: TCGG	1400 ACTC::::ACTC
1200 1210 1220 1230 1240 1250 AGCACCACCAGATAGCAGCTGGAGAGGTCTCAAAGTGCCCTACAATGTTGGACCTGG	CACATGCTCTGA-AG-GTTGGAAAGGTGCGATCCATTCCTGTAAGGT-GACAA	1260 1270 1280 1290 1300 1310 CTTTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGT	CC	1320 1330 1340 1350 1360 1370  GACAAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGA	0 1400 1410 1420 1430  CACCGGGACTCATGGTGTTTGGTGTATTGACCCTCAGAGTGGAGC  :: :::: :::: :::: :::: :::: :::::::::
729	. i	rti	9	VTG'	CCC
1210 GATA	 A-A	1270 AACT	į	30 CAA :: GAA 280	390 GTCA :: CCCA
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√CC	CTCT	) 106,	: ::: CAGGA( 1220	1320 133 GACAAGAATTTAC : ::: CAGGAAGATTCTG	1380 139 CATTCTGGGAGGT : :::: TGTGATTGGAGCC 1330 13
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1440 1450 1460 1470 1480 1490 AGCTGTTGTTGAAATTGTGAGGAGCTTTGGAACACTGAAAAGGAAGGGTGGAG :::::::::::::::::::::	1500 1510 1520 1530 1540 1550  ACCTAGAAGAACAATTTTGCTAGCTGGGATGCAGAAGTTTTGGTCTTTGGTTC ::::::::::::::::::::::	TACTGAGTGGCAGAGGAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAA :::::::::::::::::::::::::::::	1620 1630 1640 1650 1660 1670  TGC-TGACTCATCTATAGAAGGAAACTA-CACTCTGAGAGTTGATTGTACACCGCTGATG ::::::::::::::::::::::::::::::::::
1480 ACTGAAAAAC :::::::	1540 AGAATTTGGTC :::::: AGACTACGGAG 1490	1600 GCGTGGCGTG : : CAAAGCTTTC	1660 GTTGATTGTA :: : : ATTTCTGCCA
1470 1480 1490 GAGCTTTGGAACACTGAAAAAGGAAGGGTG :::::::::::::::::::::::::::::::::	1530 GGGATGCAGA :: ::: GGAGTGCAGG	1590 TCCTTCAAGA : :: :: : TGCTGCATGC	1650 CACTCTGAGA: : : : : : : : : : : : : : : : : :
1460 3TGAGGA : :: 3CCCGTGTGA 1410	1510 1520 1530 15 ATTTTGCAAGCTGGGATGCAGAATT :: X::::::::::::::::::::::::::::::::::	1580 AATTCAAGAC : :X FACTCTGCCA 1530	1640 AGGAAACTA- :::::: IGGGAGCAAG
1450 CATGAAATTGI :::::: TTGGAACTTG	1510 AACAATTTTG	1570 GCAGAGGAGAATTC :::::X CTGGAGGGGTACTC 1520 153	1630 :::: :::::::::::::::::::::::::::::::
1440 1450 1460 AGCTGTTCTTCATGAAATTGTGAG- :::::::::::::::::::::::::::::::::::	1500 ACCTAGAAGAAC ::: :: :: ACCGAGGCGAAG	1560 TACTGAGTGG :::::::: TACTGAATGG	1620 TGC-TGACTCATC:::::
pmsgen CHKTFE	pmsgen	pmsgen CHKTFE	pmsgen CHKTFE

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1730	TTGAAGGC	••	CAGAGAGC	1680	1790	GCATGCCC		GGCCTGGA	
1720	SATGAAGGCT	••	SCAGCAGTCT	1670	1780	AGTTCAGTG		GTTCCTCTT	1730
1710	AAAAGCCCTC	•••	AAGAATCCAG	1660	1770	CCTTCCCCAG		AAAAGCAGTI	1720
1700	<b>AACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGC</b>		GAAGGGGGTG	1650	1760	TAAAAAAGT	••	CTCTATAACAGACTTGGCCCAGACTGGGTAAAAGCAGTTGTTCCTCTTGGCCTGGA	1710
1690	CACAACCTAAC	••	GGGAGTATTA1	1640	1750	SAAAGTTGGAC	•••	CAGACTTGGCC	1700
1680	TACAGCTTGGTACAC	•••	TATATGCTGCTGGGGAGTATTATGAAGGGGGTGAAGAATCCAGCAGCAGTCTCAGAGAGC	1630	1740	pmsgen AAATCTCTTTATGAAAGTTGGACTAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCC	••	CTCTATAA	1690
				UTE S		pmsgen		CHKTFE	
	S	UBS	STIT	ute s	HEE	r (R	ULE	26	)

<b>-</b>	2	8/48	• •
311	-TJ	FTC	ACT
164 164	TGGCT	\TAGA1	10 \ATG \ATGTZ
164	1250 TGTTGGACC	GTTGGAAT? 660	1310 CTCT-ACCAA :::::::: CTGTGAACAA
3' end.	DAAAGTGCCCTACAATGTTGGACCTGGCTT	rgrccrccra 650	1300 GCACATC-CA : : : : : : : : : : : : : : : : : : :
tor mRNA,	1230 AGTCTCAAAG	GGAAGGAAAC 640	280       1300       1310         ACAAAAAGTCAAGATGCACATC-CACTCT-ACCAATG       ::::::::::::::::::::::::::::::::::::
rrin receptor 60 nt overlap	1220 CTGGAGAGGA	TCAAAAACATO 630	1280 TCTACACAAA ::: AACTTTCACA
TTRFR Rat transferrin receptor mRNA, 3' end 55.5% identity in 560 nt overlap	1210 CCAGATAGCAG	AGAAAAGCTAT 620	1260 1270 1280 1290 1300 1310 pmsgen -TACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATC-CACTCT-ACCAATG RATTRF CTCATGTAAGCTGGAACTTTCACAGAATCAAAATGTGAAGCTCACTGTGAACAATGTACT 670 680 690 700 710
RATTRFR F 55.5% ide	g pmsgen ccaccagaragcagcrggaggaggaggrgcrgaagrgcccracaargrrggaccrggcrr-	RATTRF TGCAGAAAAGCTATTCAAAAACATGGAAGGAAACTGTCCTCCTAGTTGGAATATAGATTC  発 610 620 630 640 650 650	

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1370 CAGACAG ::::::	1430 CTCAGAG :::: TCCAGTG	180 AAAAGGAA ::: :: CAAAAGAT	40 TGGTCTT :::::
1360 CAGTGGAACCAGACA : :::::::: ATGAGGAACCAGACC	10 1420 TTGGTGGTATTGACC :::::::: CTGGT-GTTGCGAAG	1480 -CTGAAAA ::: :ATGATTTCAA	1540 AGAAGAATTTG : :: :: :: AGGAGACTATG 960
1350 CTCTCAGAGGAGG : : ::: TTATTAAAGGCTV	1410 :::: ; :::: ; :::: ;	1470 ::::::::::::::::::::::::::::::::::::	1530 TGGGATGCA ::: ::: TGGACTGCA
1340 TAGGTACTCT : :: :: TTGGCGTTA1	1400 ACTCATGGGT:::::ACGCTTGGGG	1460 STGAGGAGCT :: CCCCAAGTA 880	1510 1520 1530 1540  CAATTTTGTTTGCAAGCTGGGATGCAGAATTTTGGT  :::::::::::::::::::::::::::
1320 1330 1340 1350 1360 1370 pmsgenAAGTGACAGTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAG :::::::::::::::::::::::::::	1380 1390 1400 1410 1420 1430 pmsgen ATATGTCATTGGGGGGTCTCATGGGTGTTTGGTGGTATTGACCCTCAGAG ::::::::::::::::::::::::::::::::::	1440 1450 1460 1470 1480 pmsgen T-GGAGCTGTTCATGAAATTGTGAGGAGCTTTGGAACA-CTGAAAAAGGAA :::::::::::::::::::::::::::	1490       1510       1520       1530       1540         GGGTGGAGACCTAGAACTTTTGTTTTGCAAGCTGGATGCAGAACTTTTGGTCTT       ::::::::::::::::::::::::::::::::::::
320 13 ACAAGAATTT :::::: ACAAGAATAC 740	80 TTCTGGGAGG : :::: TAGTAGGAGG	1440 AGCTGTTGTTC ::::::	1500 AGACCTAGAAGA X::::::::
1320 pmsgenAAGTGACAAGAATT ::: ::::: RATTRF GAAAGAAACAAGAATZ	1380 pmsgen ATATGTCATTCTGGG ::::::::::::::::::::::::::::::::	1440 T-GGAGCAGCTG:::::	1490 GGGTGGAGA :: X: S GGATTTAGA
pmsgen – RATTRF G	pmsgen antikartrr 79		pmsgen RATTRF
	3000111012 3	11LL (11ULL 2U)	

pmsgen RATTRF	1550 1 CTTGGTTCTACT ::::::::: GTTGGTCCGACT 970 98	1560 CTGAGTGGG :::::: CTGAGTGGC7 980	1550 1560 1570  CTTGGTTCTACTGAGTGGGCAGAGGAA :::::::::::::::X  GTTGGTCCGACTGAGTGGCTGGAGGGTACC 970 980 10	1580 TTCAAGACT :::: CCTTTCATCTTT 1000	1550 1560 1600 pmsgen CTTGGTTCTACTGAGTGGCAGAGGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTG	1600 GTGGCGTG : : GCTTTC 1020
pmsgen RATTRF	1610 pmsgen GCTTATATTAATG :::: ::::: RATTRF ACTTACATTAAT- 1030	1620 TGCTGACTC : ::: : T-CTGGATA 1040	1630 :ATCTATAGAAG : : : AAGTCGTCCTG	1640 GAAACTA-CAC : ::: :: GGTACTAGCAA 1060	1610 1620 1630 1640 1650 1660 GCTTATATTAATGCTGACTCTATAGAAGGAAACTA-CACTCTGAGAGTTGATAGTAC ::::::::::::::::::::::::::::::::::::	1660 GATTGTA : : TCTGCCA 1080
en 1	1670 pmsgen ACCGCTGATGTAC.	1680 ACAGCTTGG	1690 TACACAACCTA	1700 ACAAAAGAGC	1680 1690 1700 1710 1720 AGCTTGGTACAACAAAAGAGCTGAAAAGC-CCTGATGAAG	1720 TGATGAAG
₹ C	CCCCTATTATA	ATACACTTA:	: :: :: TGGGGAAGATA	: ::: ATGCAGGA	RATTRF CCCCCTATTATACACTTATGGGGAAGATAATGCAGGACGTAAAGCATCCGA-	:: CGA

3	31/48	
1730 1740 1750 1760 1770  CTTTGAAGGCAAATCTCTTTAT-GAAAGTTGGACTAAAAAAGTCCTTCCCCAG :::::::::::::::::::::::::::::::::	1780 1790 1800 1810 1820 1830 AGTTCAGTGGCATGCAGGATAAGCAAATTGGGATCTGGAAATGATTTTGAGGTGTTTCT	RATTRF CCTTGGACTTCCCTTTTTCTTGCATATTCAGGAATCCCAGCAGTTTCTTTC
1750 1760 GTTGGACTAAAAAAGT ::::::::::::::::::::::::::::::	1820 GGAAATGATTT	GGAATCCCAGC 1240
1750 AGTTGG2 : :::: :AGTAATTGG2	1810 ATTGGGATCT	rgcatattca 1230
1730 1740 pmsgen GCTTTGAAGGCAAATCTCTTTAT-GAA ::::::::::::::::::::::::::::::::	1800 GATAAGCAA	rcccrrrrcrr 1220
1740 3GCAAATCTCTT : ::::::::::::::::::::::::::::::::::	1790 GCATGCCCA(	ATGCTGCATI 1210
ΰi	1780 AGTTCAGTG	CCTTGGACA 1200
pmsgen RATTRF	pmsgen	RATTRF
SUBSTIT	'UTE SHEE'	T (RULE 26)

99		
2	CAC	CTC
145	CTA	AAC
145	1270 AAACTTTT	raggarggr 1190
cq	SGAA	TAG
complete	3ACCTGGCTTTAC-TGGAAACTTTTCTACAC	ACTCTACATO 1180
eptor mRNA, lap	1250 TGTTGGACCTG	CTGGAAAACAG 1170
MTFRR Human transferrin receptor mRNA, complete cd 145 145 266 54.3% identity in 464 nt overlap	1230 1240 1250 1260 1270 pmsgen AGGAAGTCTCAAAGTGCCTACAATGTTGGACCTGGCTTTAC-TGGAAACTTTTCTACAC	HUMTFR TATGGAAGGAGACTGTCCCTCTGAAAAAAAACAGACTCTACATGTAGGATGGTAACCTC 1140 1150 1160 1160
Human trar dentity in	1230 GAAGTCTCAA	TGGAAGGAGA( 1150
HUMTFRR 54.3% i	pmsgen AG	HUMTFR TA

1330	<b>FTACAA</b>	•••	<b>PCTTAA</b>		
1320	CACATC-CACTCT-ACCAATGAAGTGACAAGAATTTACAA	•••	<b>FGAAGCTCACTGTGAGCAATGTGCTGAAAGAGAGATAAAAATTCTTAA</b>	1250	(
	AA	••	<b>IGCTGAAA</b>	1240	1
1310	CT-ACCAATG	•••	GTGAGCAATG	1230	(
1300	ACATC-CACT	•••	GAAGCTCACT	1220	
1290	GTCAAGATGC	•••	AGAAAGCAAGAATGT	1210	
1280	pmsgen AAAAAGTCAAGATG	••	HUMTFR AGAAA	1200	
:		STI		e sh	EET

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	~	••	~	
1390	CAGAGGAGCAGTGGAACCAGACAGATATGTCATTCTGGGAGGTCA	••	TAAAGGCTTTGTAGAACCAGATCACTATGTTGTAGTTGGGGCCCA	
H	3AG	••	366	
	rGG(	••	LLC	0
0	TC		AG	1310
1380	CAT	••	TGT	
	TGT	•••	IGT	
	ATA'	••	TA	1300
370	SAG		CA(	H
137	GAC	••	<b>IGA</b>	
	222	•••	2001	0
0	GAA	••	GAA	1290
1360	GTG	•••	GTA	
	GCA		TTT	
	3GA	••	286	1280
1350	AGA(	•••	AAA	H
ä	TC	••	\TT!	
	CTC	••	TT	0
0	TGTGATAGGTACTCT	••	CATCTTTGGAGTTAT	1270
1340	TAG	••	TTG	
	<b>IGA</b>	••	TCT	
	TG'		CA	1260
	yen		JMTFR	1
	pmsgen		HUM	

	14	400	1410	1420	1430	1440	1450
pmsgen	CCGGGAC	ATGGGT	STTTGGTGG	STATTGACCC	rcagagt-g	GTTTGGTGGTATTGACCCTCAGAGT-GGAGCAGCTGTTGTTCATG	TTCATG
	••	••	••	••	•••	•••	••
HUMTFR	GAGAGAT	GAGAGATGCATGGGG	CCCTGGAGC	TGCAAAATC-	-CGGTGTAGG	CCCTGGAGCTGCAAAATC-CGGTGTAGGCACAGCTCTCCTATTGA	TATTGA
13	1320	1330	1340	1350	1360	0 1370	

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<b>AA</b> 	A :: 6	CT	AC
1460 1470 1480 1490 1500 pmsgen AAATTGTGAGGAGCTTTGGAACACTGAAAAGGAAGGGTGGAGACCTAGAACAA ::::::::::::::::::::::::::::::::	1520	1590 1600 1610 1620  ACTCCTTCAAGAGCGTGGCGTGGCTTATTAATGCTGACTCATCT :::::X :: :: :: :: TATTATATTAATGCTGATAAAGCGTCCTTCATCTTAAAAGCGATAAAGCGATAAAAGCG 1520 1530 1540 1550	1650 1660 1670 1680  CACTCTGAGAGTTGATCACCGCTGATGTACA-GCTTGGT-AC :: ::::::::::::::::::::::::::::::::::
480 1490 AAAAGGAAGGGTGGAG ::: X:: TAAAAGATGGGTTTCA	1550 rcttcttggttc :::::: \tcggttggtgc	1610 ::::::X :CACTTATATTAATGC	1670 ::::::::::::::::::::::::::::::::::::
1480 ACTGAAAAAC : ::: 3GTCTTAAAA	1530 1540 TGCAGAAGAATTTGGT ::::::::::::::::::::::::::	1600 AGCGTGGCGT : : AAAGGCTTT	1660 TGATTGTAC: : : :
1470 CTTTGGAAC :: : : CTCAGATAT	1530 GGATGCAGA/ : ::: ; SAGTGCTGG/ 1460	1590 CTCCTTCAAGA : :: :: C-CCTGCATTT	1650 CTCTGAGAGT : : :: ACTTCAAGGT
1460 TGAGGAG :::: CCCAGATGTT 1390	1520 TTTTGTTTGCAAGCTGGG :::::::::::::::::::::::::::::::::	1570 1580 A-GGAGAATTCAAGAC : :: : : : : : : : : : : : : : : : : :	1630 1640 ATAGAAGGAAACTACAG : : : :: GTTCTTGGTACCAGCAGAGTACAGCAGAAACTAGGTACCAGCAAAACTAGCAAAACTAGCAAAACTAGCAAAACTAGCAAAACTAGCAAAAACTAGCAAAAAAAA
n AAATTG :: ::: R AACTTG( 1380	1510 n TTTTGTT :: :: R TTATCTT	1570 1580 n A-GGAGAATTCAAG : ::::::::::::::::::::::::::::::::::	
pmsge HUMTF	pmsgen HUMTFR	pmsgen HUMTFR	pmsgen HUMTFR
	SUBSTITUTE SH	HEET (RULE 26)	

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1740	pmsgen ACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATG		HUMTFR AAAACAATGCAAAATGTGAAGCATCCGGTTACTGGGCAATTTCTATATCAGGACAGCAAC	1670
1730	TTTGAAGGCA		ATTTCTATAT	1660
1720	TGATGAAGGC		TTACTGGGCA	1650
1710	TGAAAAGCCC		AAGCATCCGG	1640
1700	ACAAAAGAGC	•••	SCAAAATGTG,	1630
1690	ACAACCTAA	••	AAAACAATC	1620
	pmsgen		HUMTFR	

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#### 35/48 FIGURE 17A

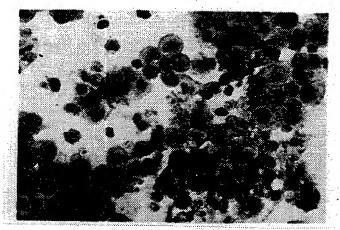


FIGURE 17B

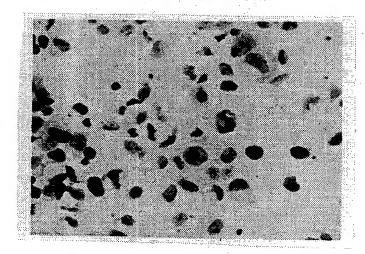
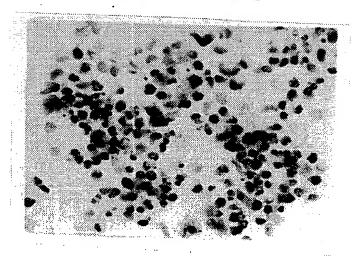


FIGURE 17C



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#### FIGURE 18

1 2 100 – 68 – 43 –

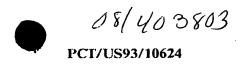
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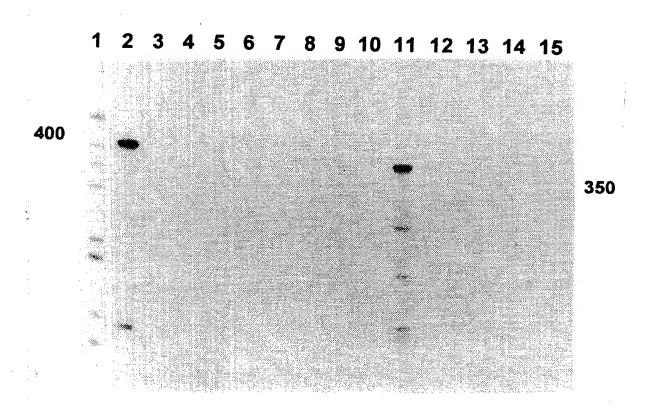
FIGURE 19

1 2 3 4

200 kDa — PSM
69 kDa —

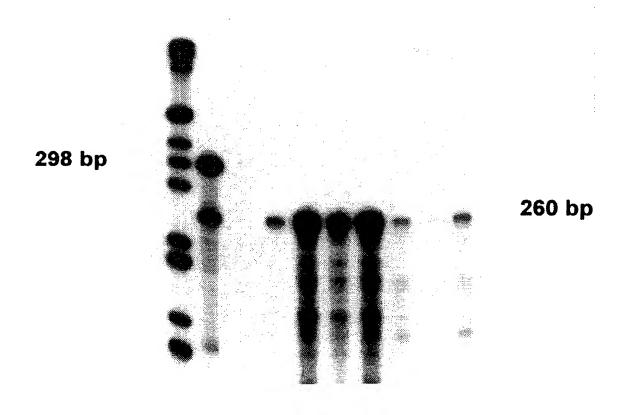


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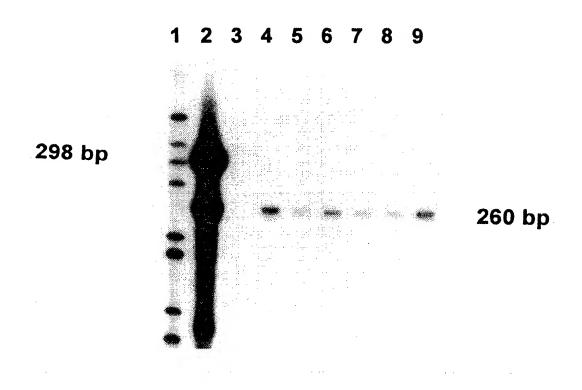


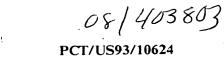
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1 2 3 4 5 6 7 8 9 10



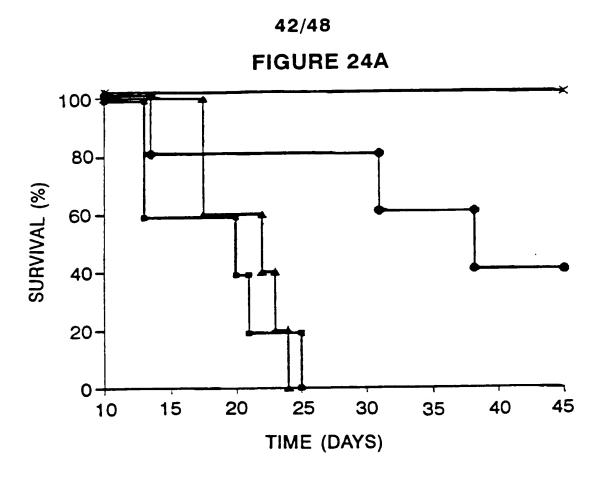
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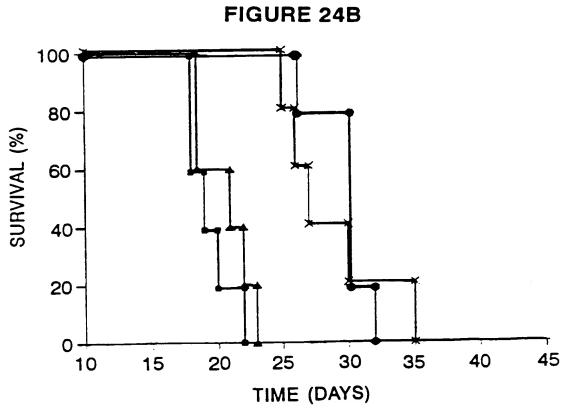




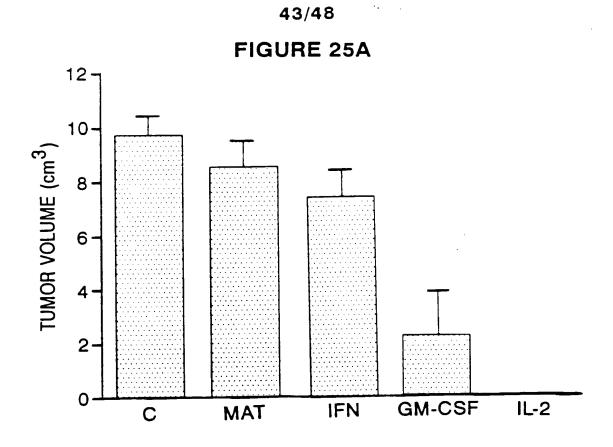
### 41/48 FIGURE 23

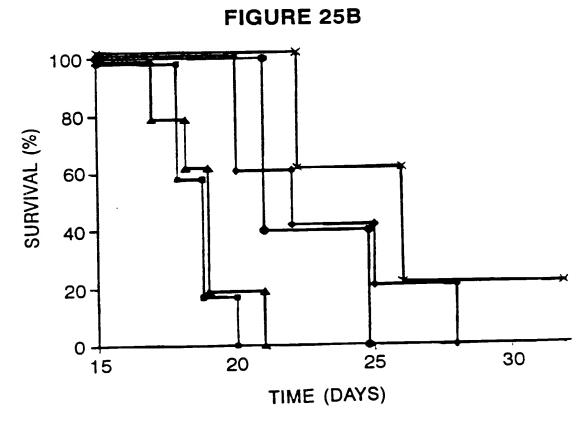
CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	_	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	_	_
R1564 (RAT MAMMARY)	NO	YES	_	-
R1564-11-c14	YES	YES	_	+
R1564-11-c15	YES	YES	_	REPEAT
R1564-11-c16	YES	YES	_	ND
R1564-11-c12	YES	YES	ND	+





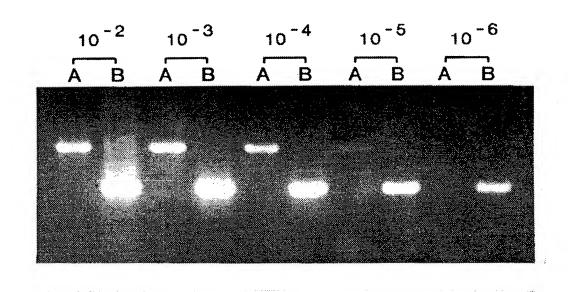
SUBSTITUTE SHEET (RULE 26)

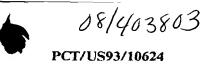




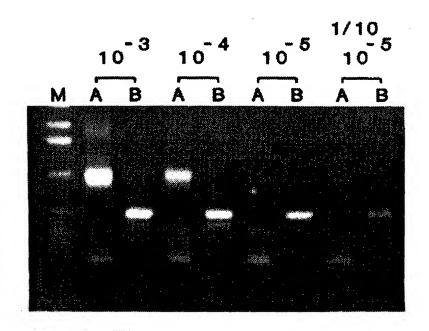
SUBSTITUTE SHEET (RULE 26)

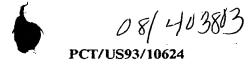
44/48 FIGURE 26



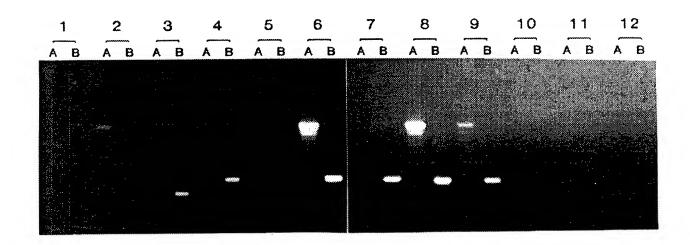


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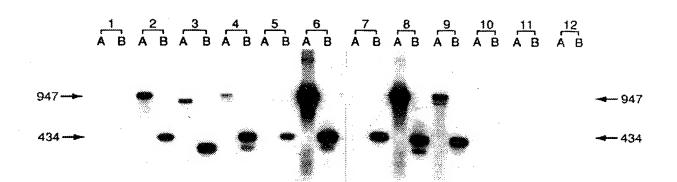
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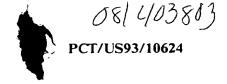




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#### 48/48 FIGURE 30

Patient	Stage	Tr_atment	PSA	PAP	PSA-PCR	PSM-PCR	
1	T2NxMo	None	8.9	0.7	-	+	
2	T2NoMo	RRP 7/93	6.1	_	-	+	
3	T2CNoMo	PLND 5/93	4.5	0.1	_	+	
4	T2BNoMo	RRP 3/92	NMA	0.4	_	+	
5	T3NxMo	Proscar + Flutamide	51.3	1.0	_	+	
6	Recur T3	I-125 1986	54.7	1.4	_	+	
7	ТЗАПОМО	RRP 10/92	NMA	0.3	_	+	
8	T3NxMo	XRT 1987	7.5	0.1	-	_	
9	T3NxMo	Proscar + Flutamide	35.4	0.7	_	-	
10	D2	S/P XRT Flutamide +Emcyt	311	4.5	+	+	
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+	
12	T2NoMo	RRP 8/91	NMA	0.5	_	+	
13	ТЗМоМо	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-		
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	-	
15	D1	Proscar + Flutamide	20.8	0.5	-	(	
16	T2CNoMo	RRP 4/92	0.1	0.3	_	-	
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